TEAM 6

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   US/08/462,355

DATE: 08/18/95
TIME: 16:03:25

INPUT SET: S5634.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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1                               SEQUENCE LISTING
2
3    (1)    General Information:
4
5         (i) APPLICANT: Coleman, Roger                    ENTERED
6                        Au-Young, Janice
7                        Bandman, Olga
8                        Seilhamer, Jeffrey J.
9
10        (ii) TITLE OF INVENTION: C5a-Like Seven Transmembrane Receptor
11
12       (iii) NUMBER OF SEQUENCES: 2
13
14        (iv) CORRESPONDENCE ADDRESS:
15             (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
16             (B) STREET: 3330 Hillview Avenue
17             (C) CITY: Palo Alto
18             (D) STATE: CA
19             (E) COUNTRY: USA
20             (F) ZIP: 94304
21
22        (v) COMPUTER READABLE FORM:
23             (A) MEDIUM TYPE: Floppy disk
24             (B) COMPUTER: IBM PC compatible
25             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28        (vi) CURRENT APPLICATION DATA:
29             (A) APPLICATION NUMBER:
30             (B) FILING DATE:
31             (C) CLASSIFICATION:
32
33      (viii) ATTORNEY/AGENT INFORMATION:
34             (A) NAME: Luther, Barbara J.
35             (B) REGISTRATION NUMBER: 33954
36             (C) REFERENCE/DOCKET NUMBER: PF-0040 US
37
38        (ix) TELECOMMUNICATION INFORMATION:
39             (A) TELEPHONE: 415-855-0555
40             (B) TELEFAX: 415-852-0195
41
42
43   (2) INFORMATION FOR SEQ ID NO:1:
44
45        (i) SEQUENCE CHARACTERISTICS:
46             (A) LENGTH: 1446 base pairs
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47                    (B) TYPE: nucleic acid
48                    (C) STRANDEDNESS: single
49                    (D) TOPOLOGY: linear
50
51          (ii) MOLECULE TYPE: cDNA
52
53
54          (vii) IMMEDIATE SOURCE:
55                    (A) LIBRARY: Mast Cell
56                    (B) CLONE: 8118
57
58
59
60          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62   ATGGCGTCTT TCTCTGCTGA GACCAATTCA ACTGACCTAC TCTCACAGCC ATGGAATGAG      60
63
64   CCCCCAGTAA TTCTCTCCAT GGTCATTCTC AGCCTTACTT TTTTACTGGG ATTGCCAGGC     120
65
66   AATGGGCTGG TGCTGTGGGT GGCTGGCCTG AAGATGCAGC GGACAGTGAA CACAATTTGG     180
67
68   TTCCTCCACC TCACCTTGGC GGACCTCCTC TGCTGCCTCT CCTTGGCCTT CTCGCTGGCT     240
69
70   CACTTGGCTC TCCAGGGACA GTGGCCCTAC GGCAGGTTCC TATGCAAGCT CATCCCCTCC     300
71
72   ATCATTGTCC TCAACATGTT TGGCAGTGTC TTCCTGCTTA CTGCCATTAG CCTGGATCGC     360
73
74   TGTCTTGTGG TATTCAAGCC AATCTGGTGT CAGAATCATC GCAATGTAGG GATGGCCTGC     420
75
76   TCTATCTGTG GATGTATCTG GGTGGTGGCT TTTGTGTTGT GCATTCCTGT GTTCGTGTAC     480
77
78   CGGGAAATCT TCACTACAGA CAACCATAAT AGATGTGGCT ACAAATTTGG TCTCTCCAGC     540
79
80   TCATTAGATT ATCCAGACTT TTATGGGGAT CCACTAGAAA ACAGGTCTCT TGAAAACATT     600
81
82   GTTCAGCCGC CTGGAGAAAT GAATGATAGG TTAGATCCTT CCTCTTTCCA AACAAATGAT     660
83
84   CATCCTTGGA CAGTCCCCAC TGTCTTCCAA CCTCAAACAT TTCAAAGACC TTCTGCAGAT     720
85
86   TCACTCCCTA GGGGTTCTGC TAGGTTAACA AGTCAAAATC TGTATTCTAA TGTATTTAAA     780
87
88   CCTGCTGATG TGGTCTCACC TAAAATCCCC AGTGGGTTTC CTATTGAAGA TCACGAAACC     840
89
90   AGCCCACTGG ATAACTCTGA TGCTTTTCTC TCTACTCATT TAAAGCTGTT CCCTAGCGCT     900
91
92   TCTAGCAATT CCTTCTACGA GTCTGAGCTA CCACAAGGTT TCCAGGATTA TTACAATTTA     960
93
94   GGCCAATTCA CAGATGACGA TCAAGTGCCA ACACCCCTCG TGGCAATAAC GATCACTAGG    1020
95
96   CTAGTGGTGG GTTTCCTGCT GCCCTCTGTT ATCATGATAG CCTGTTACAG CTTCATTGTC    1080
97
98   TTCCGAATGC AAAGGGGCCG CTTCGCCAAG TCTCAGAGCA AAACCTTTCG AGTGGCCGTG    1140
99
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100  GTGGTGGTGG CTGTCTTTCT TGTCTGCTGG ACTCCATACC ACATTTGGGG AGTCCTGTCA  1200
101
102  TTGCTTACTG ACCCAGAAAC TCCCTTGGGG AAAACTCTGA TGTCCTGGGA TCATGTATGC  1260
103
104  ATTGCTCTAG CATCTGCCAA TAGTTGCTTT AATCCCTTCC TTTATGCCCT CTTGGGGAAA  1320
105
106  GATTTTAGGA AGAAAGCAAG GCAGTCCATT CAGGGAATTC TGGAGGCAGC CTTCAGTGAG  1380
107
108  GAGCTCACAC GTTCCACCCA CTGTCCCTCA AACAATGTCA TTTCAGAAAG AAATAGTACA  1440
109
110  ACTGTG                                                            1446
111
112
113
114  (2) INFORMATION FOR SEQ ID NO:2:
115
116         (i) SEQUENCE CHARACTERISTICS:
117               (A) LENGTH: 482 amino acids
118               (B) TYPE: amino acid
119               (D) TOPOLOGY: linear
120
121         (ii) MOLECULE TYPE: protein
122
123         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
124
125  Met Ala Ser Phe Ser Ala Glu Thr Asn Ser Thr Asp Leu Leu Ser Gln
126   1               5                  10                  15
127
128  Pro Trp Asn Glu Pro Pro Val Ile Leu Ser Met Val Ile Leu Ser Leu
129              20                  25                  30
130
131  Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala
132          35                  40                  45
133
134  Gly Leu Lys Met Gln Arg Thr Val Asn Thr Ile Trp Phe Leu His Leu
135       50                  55                  60
136
137  Thr Leu Ala Asp Leu Leu Cys Cys Leu Ser Leu Ala Phe Ser Leu Ala
138   65                  70                  75                  80
139
140  His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys
141              85                  90                  95
142
143  Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Gly Ser Val Phe Leu
144              100                 105                 110
145
146  Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile
147          115                 120                 125
148
149  Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly
150       130                 135                 140
151
152  Cys Ile Trp Val Val Ala Phe Val Leu Cys Ile Pro Val Phe Val Tyr
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153    145                      150                    155                    160
154
155    Arg Glu Ile Phe Thr Thr Asp Asn His Asn Arg Cys Gly Tyr Lys Phe
156                    165                    170                    175
157
158    Gly Leu Ser Ser Ser Leu Asp Tyr Pro Asp Phe Tyr Gly Asp Pro Leu
159                    180                    185                    190
160
161    Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn
162            195                    200                    205
163
164    Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr
165            210                    215                    220
166
167    Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp
168    225                    230                    235                    240
169
170    Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser
171                    245                    250                    255
172
173    Asn Val Phe Lys Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly
174                    260                    265                    270
175
176    Phe Pro Ile Glu Asp His Glu Thr Ser Pro Leu Asp Asn Ser Asp Ala
177            275                    280                    285
178
179    Phe Leu Ser Thr His Leu Lys Leu Phe Pro Ser Ala Ser Ser Asn Ser
180            290                    295                    300
181
182    Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu
183    305                    310                    315                    320
184
185    Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile
186                    325                    330                    335
187
188    Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met
189                    340                    345                    350
190
191    Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe
192            355                    360                    365
193
194    Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Val Ala
195            370                    375                    380
196
197    Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Trp Gly Val Leu Ser
198    385                    390                    395                    400
199
200    Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp
201                    405                    410                    415
202
203    Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro
204            420                    425                    430
205
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```
206   Phe Leu Tyr Ala Leu Leu Gly Lys Asp Phe Arg Lys Lys Ala Arg Gln
207           435             440             445
208
209   Ser Ile Gln Gly Ile Leu Glu Ala Ala Phe Ser Glu Glu Leu Thr Arg
210       450             455             460
211
212   Ser Thr His Cys Pro Ser Asn Asn Val Ile Ser Glu Arg Asn Ser Thr
213   465             470             475             480
214
215   Thr Val
216
217
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/462,355*

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